# OPENING THE RESEARCHER'S WORLD TO SCHOOL STUDENTS

by **Ken Eames, Jenny Gage, Andrew Conlan, Adam Kucharski and Julia Gog**

Carrying out scientific research is a rewarding and enlightening experience, and there is no reason why it should be the sole preserve of professional scientists in universities and research labs. Here we describe a partnership between a group of research scientists (initially based at the University of Cambridge) and 14 secondary schools, assisted by the Millennium Mathematics Project, University of Cambridge. Students at schools around the UK have been working closely with the researchers to design and carry out a research project, collecting data to help us understand social mixing patterns and the spread of infectious diseases.

In this article we describe how this project has enabled secondary school students to play an active part as researchers, strengthening links with local primary schools in the process. Motivated by hands-on examples of mathematical models of epidemics, the research explores ideas of chance, variation, and social networks. The resources used in the project are freely available for teachers to use with their own students.

## Mathematical Models, Mixing Patterns, and the Spread of Disease

As all parents and teachers know, schoolchildren are at particular risk of infection. The main driving force of a wide range of diseases is their spread among children, from the historical childhood infectious diseases, such as measles and mumps, through to current high-profile examples such as influenza. There are several reasons for this. First, many infections confer immunity, so most adults are already immune whereas children, previously unexposed, are still susceptible. Second, children make far more social contacts than adults, so are more likely to encounter infection. Third, children's social contacts are generally with other children, further concentrating the risk of infection.

Mathematical models of infectious disease spread have long been used to explain observed patterns of incidence and, increasingly, to test control strategies (Keeling and Rohani, 2007). Models are used to aid decisions about vaccination, providing guidance about which age groups should be targeted, and what level of coverage is necessary. Recently, models have been used to investigate whether it would make sense to vaccinate schoolchildren against flu in order to protect vulnerable adults (Baguelin *et al*., 2010).

While no model can ever capture all the details of the real world, good models, grounded in high quality data, are extremely useful public health tools – something that we want to make students aware of, so that they realize the importance of maths in the real world.

Because children are such a significant factor in the spread of infectious diseases, information about the social mixing patterns of children is an important aspect of mathematical models of disease spread. An influential study of mixing patterns in eight European countries (Mossong *et al*., 2008) demonstrated the high levels of social mixing amongst children. It also showed, perhaps not surprisingly, that most of their contacts were with children of a similar age. These data have become an integral part of infectious disease modelling (Baguelin *et al*., 2010; Rohani *et al*., 2010), but modellers would like to have better information about whom children mix with in their own schools, and whom they mix with from other schools. It is likely that social networks and friendship groups within schools and within classes are key factors influencing patterns of disease transmission. It is also clear that mixing behaviour in school term time and holidays will be different (Eames *et al*., 2012). In our work with schools, we have been collecting data that will help us to find out more about these crucial factors.

Collecting reliable social mixing data from school-children, particularly primary schoolchildren, is challenging. Surveys designed by adults for adults are unlikely to be suitable for completion by younger children, so are generally completed by parents. Whilst these data are useful, inevitably they miss a great deal of detail, particularly where school social networks are concerned. Our first challenge therefore was to design a study that asked the right questions in the right ways. The second was to recruit children to take part in the study.

As university-based researchers, we felt we were not in the best position to meet these challenges. However, by working directly with secondary school students we benefitted from their help in designing a questionnaire and facilitating its use with primary schoolchildren. So far we have carried out two phases of the project, repeating each phase over two consecutive school years.

## Research Projects in Schools

The first phase focused on social networks of primary schoolchildren in school. Two secondary schools were involved in the first year, and four in the second. These six secondary schools recruited a total of 75 classes, from Reception to Year 6, in 11 primary schools, with almost 90% of the primary children completing questionnaires.

The second phase is now in its second year. It focuses on differences between holiday and term time movement patterns, with four secondary schools involved each year.

Communication with the secondary schools has been through videoconferencing. Videoconferences with the students take place roughly every 2 months, following an initial teacher briefing. In each videoconference, there is an opportunity for the students to feedback on what they have done since the previous session, to learn more about the spread of disease and the research process, and to be briefed on the next stage of the project. In both phases of the project, students have been expected to take an active role in designing and implementing a survey, and analysing their data.

We have used a variety of simple models to help explain how mathematical modelling works and how it can be used to help predict the progress of an infectious disease. These models are freely available on the NRICH (**nrich.maths.org**) website in the Disease Dynamics Schools' Pack [**maths.org/DiseaseDynamics**].

## What We've Learnt so Far

From a research perspective, the project has been extremely successful. Thanks to the expertise, enthusiasm and hard work of the secondary school researchers, we have been able to collect a large amount of new data about social mixing in primary schools. For the first time in a large-scale study, we have been able to measure detailed social networks in primary schools, confirming what teachers may well already know, but, importantly, quantifying that knowledge.

The children's networks displayed highly clustered friendship groups within classes, and strong levels of segregation by gender, with effects appearing to be greatest amongst older pupils (Fig. 1). In primary schools with more than one class per year group, the majority of reported between-class contacts were with children in the same year group.

It is clear that schools are not 'well-mixed' environments for the spread of infections, so social structure both within and between classes is important for understanding patterns of transmission. These results have been described in detail elsewhere (Conlan *et al.*, 2011).

Preliminary results from the second phase suggest that we have been able to measure movement patterns successfully. We have seen marked differences between

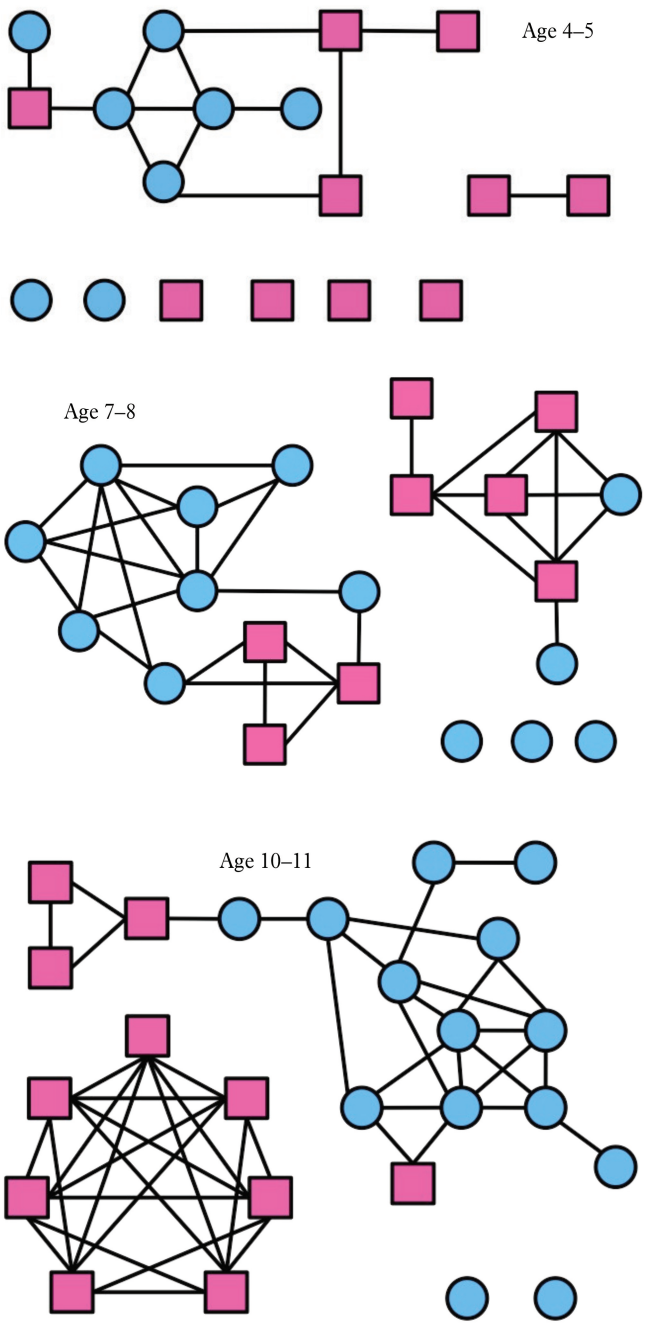


**Fig. 1** Example networks measured in three primary school classes. Individuals are connected in the network only if each reported the other as a contact. Girls are shown as pink squares, boys as blue circles. Figure adapted from Conlan *et al.* (2011).

regular, local, movements during term time and less predictable, long distance, movements during school holidays.

## Models and Activities

The Disease Dynamics Schools Pack [**maths.org/DiseaseDynamics**] contains presentations about the spread of infectious diseases past and present, and mathematical models using a range of mathematical ideas. These resources provide simple practical experiments and simulations to help students explore how

diseases spread and terminate in a population. Students are encouraged to critique the models, asking how far they correspond to reality, and where they fall short. The pack provides enrichment for the data-handling and probability areas of the secondary mathematics curriculum, and topics such as epidemiology in the science curriculum.

## (i) Standing Disease

The first example is the *Standing Disease*, a disease that causes the infected person to stand up. In this model, everyone starts sitting down, and one person is chosen as the first case to initiate the epidemic. Each newly infected person stands up and chooses two of the people still sitting down to 'infect'. The number of 'cases' doubles each generation, from 1, to 2, to 4, etc., resulting in an entire class of 30 being infected within five generations of infection. Although very simple, this is a powerful visual demonstration of the early exponential growth phase of many epidemics (Fig. 2).

We can use the *Standing Disease* to help students understand the impact of vaccination: if we want to prevent an epidemic from taking off, then we must vaccinate enough people so that each infected person causes no more than one secondary case. In the *Standing Disease*, we see that we must vaccinate half the population. More generally, if each infected person causes $R$ secondary cases, we must vaccinate $(R - 1)$ of these, or a fraction $(1 - 1/R)$ of the population. This 'herd immunity' threshold is central to many vaccination programmes.

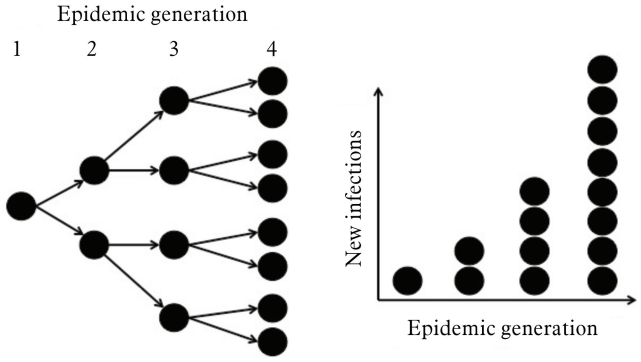


**Fig. 2** The *Standing Disease*, demonstrating the exponential early growth of an epidemic.

## (ii) Network Disease

To make models more realistic and therefore more useful, additional complexity is added step by step. The first step creates a *Network Disease*. Before the epidemic begins, each pupil writes down the names of two other people in the class: these will be the people they attempt to 'infect'. Although it begins in the same way as the *Standing Disease*, the *Network Disease* slows down once names start to be repeated (Fig. 3). This matches what happens in real epidemics as the number of susceptible

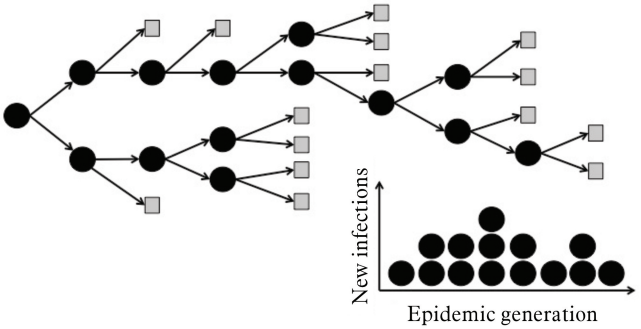


**Fig. 3** The *Network Disease*, where spread is slowed by the encounters that infectious people make with people who have already been infected. In the epidemic shown, dead ends (people previously infected) are shown as grey squares. The build-up of immunity in this model reduces the spread of the epidemic.

people in the population falls. It also mimics the reality that an individual's exposure to infection will depend to a great extent on their social contacts.

Both the *Standing Disease* and the *Network Disease* are deterministic – once they have begun, they are entirely predictable. In real outbreaks, however, chance plays an important role.

## (iii) Counterplague

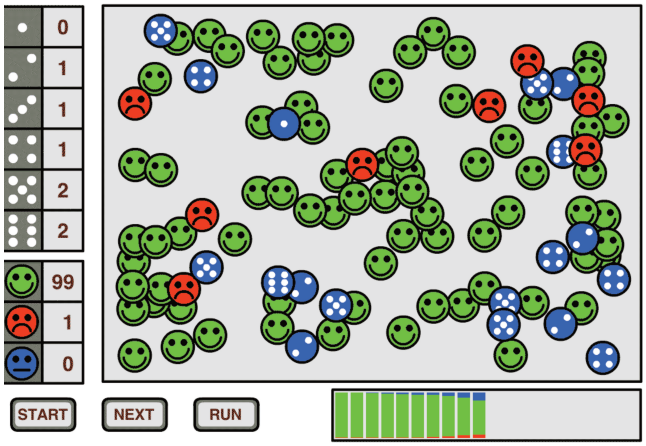


**Fig. 4** *Counterplague*, a model including chance effects in the number of infections. Susceptible individuals are shown in green, infected individuals in red, and recovered/immune individuals in blue.

The role of chance is included in the *Counterplague* model. Epidemics can be simulated using dice and counters, or an electronic version is available in the Disease Dynamics pack (Fig. 4). Here, the epidemic starts with 1 case in a population of 99 susceptible individuals. Whether an infected person infects others, and how many, depends on the simulated throw of a die – the dice on the left indicate how many new cases result from each outcome. At the point shown in Figure 4, this epidemic is gathering pace, but will cases die out before

everyone has succumbed? Students can analyse what is likely to happen by considering the average number of cases caused by an infected individual. If it is greater than 1 the epidemic is likely to grow, whereas if it is less than 1, it is likely to decrease. In this example, the expected number of new cases each infection causes is

$$0\times\frac{1}{6}+1\times\frac{1}{6}+1\times\frac{1}{6}+1\times\frac{1}{6}+2\times\frac{1}{6}+2\times\frac{1}{6}=\frac{7}{6}$$

so we would expect the epidemic to continue until everyone has been infected – which is indeed what happened!

In a more realistic adaptation of the model (*Counterplague +*, available online), numbers on the dice show not how many cases each infected person causes, but how many people they *try* to infect. As with the *Network Disease*, anyone who has previously been infected is immune to further infection; even if the epidemic initially grows quickly, 'wasted' encounters mean that it usually dies out before everyone in the population has been infected – as we see in reality.

In the final model we have used, the 'local' spread of infection is modelled using counters on a chessboard. In this model, infection can only spread to neighbouring squares, and the spatial structure of the population constrains epidemic behaviour. By including in the population some counters of a different colour, representing vaccinated individuals, we see that susceptible individuals can be protected from infection by their vaccinated neighbours – an important consideration for those who cannot be vaccinated for some reason.

## Final Comments

As researchers, we have found this project extremely rewarding, giving us the opportunity to talk about our research interests to a completely different audience. It has been valuable for us to find ways of explaining complex ideas without resorting to complicated algebra. Indeed we have been repeatedly surprised and delighted at how schoolchildren can grasp rather subtle mathematical ideas if they are offered in a real-world context, such as in disease spread and social networks. It was pleasing that so much progress could be made, and so many important concepts covered, using fairly simple models and simple materials. These are further developed in the *Maths and Our Health* packs, freely available on NRICH at **maths.org/MathsHealth**.

We have been fortunate to have the enthusiastic participation of so many groups of school pupils and their teachers, and are glad to be able to report that so far everyone has found the activities interesting and worthwhile.

When discussing these activities with colleagues, we describe them variously as research, or collaboration, or public engagement; in reality, they have been all three, and are all the more valuable for that.

As these projects have demonstrated, there is no barrier to school pupils working alongside research scientists, and nothing to stop pupils from making valuable contributions to – indeed, to guiding – cutting edge research. We would encourage everyone to get involved.


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